Epperson
09/804481

-key terms

(FILE 'HCAPLUS' ENTERED AT 11:25:08 ON 03 JUN 2003)
L1 2790 SEA FILE=HCAPLUS ABB=ON PLU=ON SNRNA OR (SN OR SMALL NUCLEAR)(W)(RNA OR RIBONUCLEIC OR RIBO NUCLEIC)
L2 852 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 AND (DNA OR DEOXYRIBO NUCLEIC OR DEOXY(W)(RIBONUCLEIC OR RIBO NUCLEIC) OR DEOXYRIBO NUCLEIC)
L3 29 SEA FILE=HCAPLUS ABB=ON PLU=ON L2 AND (BAE(W)(1 OR I) OR BAEI OR BAE1 OR RESTRICT?(W)(ENZYM? OR FRAG# OR FRAGMENT? OR SITE))

L3 ANSWER 1 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:368936 HCAPLUS
DOCUMENT NUMBER: 136:396937
TITLE: Vectors for **small nuclear RNA** library creation and uses
INVENTOR(S): De Graaf, David; Lander, Eric S.
PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA
SOURCE: U.S. Pat. Appl. Publ., 18 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002058287	A1	20020516	US 2001-804481	20010312

PRIORITY APPLN. INFO.: US 2000-188304P P 20000310

AB The present invention relates to a recombinant vector comprising an isolated **DNA** sequence encoding an **snRNA** (e.g., U1), wherein the **snRNA** sequence has been modified to contain one or more **restriction sites** such that digestion with at least one **restriction enzyme**, and preferably only one **restriction enzyme** (e.g., **Bae 1**), allows easy insertion of target-specific sequences (inserts). According to the invention, a recombinant vector comprising a **DNA** sequence encoding a **snRNA** is modified to contain one or more **restriction sites** within the **snRNA** sequence such that digestion with at least one **restriction enzyme**, and preferably only one **restriction enzyme**, produces a double-stranded **restriction fragment** with single-stranded overhangs at each end. Excision of this **restriction fragment** from **DNA** contained in the vector forms insertion sites in the **snRNA** **DNA** of the vector; these insertion sites comprise single-stranded overhangs which are complementary to the single-stranded overhangs of the **restriction fragment**. These sites readily allow the directed placement of an insertion cassette comprising a double-stranded modification fragment contg. a preselected **DNA** sequence. The vector permits the rapid and efficient creation of large libraries contg. an array of preselected sequence modifications, so that optimally-performing sequences can be quickly detected and utilized. Methods of producing recombinant vectors, and methods of utilizing the vectors to create cell libraries, to identify **snRNAs** which suppress expression of transcription products, to suppress expression of transcription products and to deliver antisense

targeting sequences are also within the scope of the invention. A sequence directed against bases 1547-1556 of luciferase was cloned into the U1/**Bae 1** vector. This construct, Luc-1547-(SEQ ID NO: 6), was cotransfected with luciferase and gave a consistent downregulation of luciferase activity by approx. 20 % (FIG. 3).

L3 ANSWER 2 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:743264 HCAPLUS
DOCUMENT NUMBER: 136:35600
TITLE: Multipoint imprinting analysis indicates a common precursor cell for gonadal and nongonadal pediatric germ cell tumors
AUTHOR(S): Schneider, Dominik T.; Schuster, Amy E.; Fritsch, Michael K.; Hu, Jie; Olson, Thomas; Lauer, Stephen; Gobel, Ulrich; Perlman, Elizabeth J.
CORPORATE SOURCE: Pediatric Oncology Group, Division of Pediatric Pathology, Department of Pathology, Johns Hopkins Medical Institutions, Baltimore, MD, 21287, USA; German Pediatric Germ Cell Tumor Study Group
SOURCE: Cancer Research (2001), 61(19), 7268-7276
CODEN: CNREA8; ISSN: 0008-5472
PUBLISHER: American Association for Cancer Research
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Pediatric germ cell tumors (GCTs) commonly arise at extragonadal sites. It has been proposed that nongonadal GCTs arise from ectopic primordial germ cells that have aberrantly migrated during embryogenesis. During a time between their migration and development to mature gametes, primordial germ cells are characterized by their lack of imprinting, which can be assessed by the evaluation of allelic gene expression and **DNA** methylation in differentially methylated control regions. To elucidate the cellular origin of nongonadal GCTs, the authors evaluated the imprinting status of 21 gonadal and 21 nongonadal pediatric GCTs. Allele-specific H19 and IGF-2 expression was assessed with reverse transcription-PCR followed by digestion at polymorphic **restriction sites**. **DNA** methylation was evaluated after bisulfite modification, PCR amplification, and restriction digestion at a consistently methylated CpG dinucleotide within the 5' flanking region of the SNRPN gene. These results were compared with genetic gains and losses detd. by comparative genomic hybridization. Seven of 15 informative tumors showed biallelic H19 expression, and 8 of 17 informative tumors showed biallelic IGF-2 expression. The frequency of biallelic gene expression was comparable in gonadal and nongonadal GCTs. Sixteen of 19 gonadal GCTs and 17 of 21 nongonadal GCTs showed absence of methylation of SNRPN consistent with loss of imprinting. One testicular GCT and three nongonadal GCTs showed a somatic methylation pattern. Two ovarian teratomas and one mediastinal teratoma showed only methylated SNRPN, consistent with entry into meiosis. Twenty-one of 22 non-GCT control samples showed a somatic methylation pattern. Gonadal and nongonadal germ cell tumors are derived from primordial germ cells that have consistently lost the imprinting of SNRPN and partly lost imprinting of H19 and IGF-2. Because the imprinting pattern of the latter genes differs

from that found in testicular GCTs of adult patients, the authors' data suggest that pediatric GCTs arise from a different stage of germ cell development.
REFERENCE COUNT: 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:637197 HCAPLUS
TITLE: Structural nucleic acids microarray
AUTHOR(S): Gagna, Claude E.
CORPORATE SOURCE: Allied Health & Life Sciences, New York Institute of Technology, Old Westbury, NY, 11568, USA
SOURCE: Abstracts of Papers, 222nd ACS National Meeting, Chicago, IL, United States, August 26-30, 2001 (2001), BIOL-186. American Chemical Society: Washington, D. C.
CODEN: 69BUZP
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB A novel technique has been developed which should accelerate basic biomedical research. This microarray system uses different double-stranded (ds-) (and single-stranded) **DNA** and RNA mols. of various base pairs. The technol. can be applied to 96-, 384-, or 1,536- well microplates. The mols., low or high m.w., are either in the right-handed (ex: A-**DNA**, B-**DNA**, A-RNA) or left-handed (ex:Z-**DNA**, Z-RNA) ds-conformations. Other nucleic acids are also used: genomic or viral **DNA**, **DNA**-RNA hybrids, methylated nucleic acids, modified & specialty nucleosides (nucleotides), bases, T-**DNA**, C-**DNA**, t-RNA, r-RNA, m-RNA, snRNP, **snRNA**, hnRNA, catalytic RNA, kinked **DNA**, bent **DNA**, nucleic acid junctions, plasmid **DNA**, pos. and neg. supercoiled **DNA**, **DNA** knots, catenanes, PCR & **restriction fragments**, and cruciform, slipped, mispaired, nodule, parallel-stranded and anisomorphic **DNAs**. Normal and diseased genes (adult & embryonic), introns, exons, operons, TATA boxes, solenoids, Okazaki fragments, promoters, replicons, replication forks, oligodeoxynucleotides, oligoribonucleotides, polynucleotides, polyribonucleotides, triplex **DNA**, quadruplex **DNA** and pentaplex **DNA**, along with many others, can be examd. Addnl., nucleic acid-protein complexes, drug intercalations and crosslinking are also used. This sensitive microarray will allow for anal. of nucleic acid geometry and dynamics.

L3 ANSWER 4 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:682435 HCAPLUS
DOCUMENT NUMBER: 134:158303
TITLE: The 28S-18S rDNA intergenic spacer from Crithidia fasciculata: repeated sequences, length heterogeneity, putative processing sites and potential interactions between U3 small nucleolar RNA and the ribosomal RNA precursor
AUTHOR(S): Schnare, Murray N.; Collings, James C.; Spencer, David F.; Gray, Michael W.
CORPORATE SOURCE: Department of Biochemistry and Molecular

Biology, Dalhousie University, Halifax, NS, B3H 4H7, Can.
SOURCE: Nucleic Acids Research (2000), 28(18), 3452-3461
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In Crithidia fasciculata, the rRNA gene repeats range in size from -11 to 12 kb. This length heterogeneity is localized to a region of the intergenic spacer (IGS) that contains tandemly repeated copies of a 19mer sequence. The IGS also contains four copies of an -55 nt repeat that has an internal inverted repeat and is also present in the IGS of Leishmania species. We have mapped the C. fasciculata transcription initiation site as well as two other reverse transcriptase stop sites that may be analogous to the A0 and A' pre-rRNA processing sites within the 5' external transcribed spacer (ETS) of other eukaryotes. Features that could influence processing at these sites include two stretches of conserved primary sequence and three secondary structure elements present in the 5' ETS. We also characterized the C. fasciculata U3 snoRNA, which has the potential for base-pairing with pre-rRNA sequences. Finally, we demonstrate that biosynthesis of large subunit rRNA in both C. fasciculata and Trypanosoma brucei involves 3'-terminal addn. of three A residues that are not present in the corresponding **DNA** sequences.
REFERENCE COUNT: 86 THERE ARE 86 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 5 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:48824 HCAPLUS
DOCUMENT NUMBER: 130:120443
TITLE: Improved methods for the detection of genomic imprinting disorders
INVENTOR(S): Nicholls, Robert D.; Saitoh, Shinji
PATENT ASSIGNEE(S): Case Western Reserve University, USA
SOURCE: PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9901580	A1	19990114	WO 1998-US13818	19980702
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9883816	A1	19990125	AU 1998-83816	19980702

PRIORITY APPLN. INFO.: US 1997-887569 A 19970703
WO 1998-US13818 W 19980702

AB The present invention relates to methods and compns. for detecting genetic abnormalities assocd. with genomic imprinting disorders. Genomic imprinting results from the preferential expression of one parental allele over the other, and defects in imprinting have been assocd. with severe developmental disorders, including Prader-Willi syndrome, Angelman syndrome, Beckwith-Wiedemann syndrome, and several types of tumors. Provided are methods and compns. for the rapid comparison of methylation patterns in **DNA** samples. The invention makes use of methylation-sensitive **restriction enzymes** and **DNA** amplification to assay the abnormal loss or acquisition of methylated **DNA** in chromosomes. The invention allows for rapid and simultaneous diagnosis of each of the major genotypic forms of Angelman and Prader-Willi syndromes and is optimal for their initial diagnosis, confirmation of a suspected clin. diagnosis, and application to population-based screening for these syndromes. It is contemplated that the methods and compns. of the presently claimed invention will find widespread use for rapid diagnosis of many of the syndromes related to genomic imprinting, including cancer.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 6 OF 29 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1997:248964 HCAPLUS

DOCUMENT NUMBER: 126:313078

TITLE: Concerted evolution of the tandemly repeated genes encoding human U2 **snRNA** (the RNU2 locus) involves rapid intrachromosomal homogenization and rare interchromosomal gene conversion

AUTHOR(S): Liao, Daiqing; Pavelitz, Thomas; Kidd, Judith R.; Kidd, Kenneth K.; Weiner, Alan M.

CORPORATE SOURCE: Dep. Molecular Biophysics and Biochem., Genetics, Yale Univ. Sch. Med., New Haven, CT, 06510-8024, USA

SOURCE: EMBO Journal (1997), 16(3), 588-598
CODEN: EMJODG; ISSN: 0261-4189

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have surveyed the tandemly repeated genes encoding U2 **snRNA** in a diverse panel of humans. We found only two polymorphisms within the u2 repeat unit: a SacI polymorphism (alleles SacI+ or SacI-) and a CT microsatellite polymorphism (alleles CT+ or CT-). Surprisingly, individual U2 tandem arrays are entirely SacI+ or SacI-, and entirely CT+ or CT-, although the SacI and CT alleles can occur in any combination. We also found that polymorphisms in the left and right junction regions flanking the tandem array fall into only two haplotypes (JL+ and JL-, JR+ and JR-). Most surprisingly, JL+ is always assocd. with JR+, and JL- with JR-. Thus individual U2 arrays do not exchange flanking markers, despite independent assortment and subsequent homogenization of the SacI and CT alleles within the U2 repeat units. We propose that the primary driving force for concerted evolution of the tandem U2 genes is intrachromosomal homogenization; interchromosomal genetic exchanges are much rarer, and reciprocal nonsister chromatid exchange apparently does not occur. Thus

concerted evolution of the U2 tandem array occurs in situ along a chromosome lineage, and linkage disequil. between sequences flanking the U2 array may persist for long periods of time.

L3 ANSWER 7 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:156332 HCAPLUS
DOCUMENT NUMBER: 124:228314
TITLE: Maintenance of imprinting of the insulin-like growth factor II gene (IGF2) and the small nuclear ribonucleoprotein polypeptide N gene (SNRPN) in the human uterus and leiomyoma
AUTHOR(S): Hashimoto, Kazumasa; Azuma, Chihiro; Kamiura, Shoji; Koyama, Masayasu; Nobunaga, Toshikatsu; Tokugawa, Yoshihiro; Kimura, Tadashi; Kubota, Yasue; Sawai, Keisuke; Saji, Fumitaka
CORPORATE SOURCE: Medical School, Osaka University, Osaka, Japan
SOURCE: Gynecologic and Obstetric Investigation (1996), 41(1), 50-4
CODEN: GOBIDS; ISSN: 0378-7346
PUBLISHER: Karger
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The insulin-like growth factor II gene (IGF2) is thought to be involved in the growth of uterine smooth muscle tumors. The authors studied the allele-specific expression of IGF2 in 20 patients with uterine leiomyomas by analyzing **restriction fragment** length polymorphisms (RFLP), because IGF2 is a maternally imprinted gene and only the paternal allele is exclusively expressed in human somatic tissue. The authors also studied the allelic expression of the small nuclear ribonucleoprotein polypeptide N gene (SNRPN), which is reportedly maternally imprinted in humans, and compared the imprinting status with that of IGF2. Nine patients (45%) were heterozygous at the ApaI site of IGF2, nine (45%) were heterozygous at the possible AccII polymorphic site of SNRPN, and three (15%) showed polymorphism in both genes. The genomic **DNA** of 15 patients showed heterozygosity in either or both of these genes, and the mRNA of these was expressed monoallelically in myometrial tissues and leiomyomas of these patients. These results demonstrated that IGF2 and SNRPN imprinting is completely maintained in human uteri and leiomyomas and that increased expression of IGF2 is not due to biallelic expression.

L3 ANSWER 8 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:551472 HCAPLUS
DOCUMENT NUMBER: 121:151472
TITLE: The spliceosomal U **small nuclear RNAs** of Ascaris lumbricoides
AUTHOR(S): Shambaugh, Joseph D.; Hannon, Gretchen E.; Nilsen, Timothy W.
CORPORATE SOURCE: Center for Molecular Parasitology, Department of Molecular Biology and Microbiology, Case Western Reserve University School of Medicine, 10900 Euclid Avenue, Cleveland, OH, 44106, USA
SOURCE: Molecular and Biochemical Parasitology (1994), 64(2), 349-52
CODEN: MBIPDP; ISSN: 0166-6851

DOCUMENT TYPE: Journal
LANGUAGE: English
AB The spliceosomal U **snRNAs** in the parasitic nematode, Ascaris lumbricoides, were isolated and characterized from a genomic library. Four potential U1 genes were clustered on a 6-kb **restriction fragment**; only 2 of the 4 genes were highly expressed. Give potential U2 **snRNA** genes were found, 4 on a single clone; the 4 genes were arranged as identical pairs on either side of an extremely long inverted repeat and only one of each pair of genes was expressed. U4, U5, and U6 **snRNA** genes were also sequenced, and the U6 promoter was characterized by block-replacement site-directed mutagenesis. With the exception of U6 (transcribed by RNA polymerase III) and the U2 pseudogenes (not transcribed), all of the genes are actively transcribed by RNA polymerase II in vitro.

L3 ANSWER 9 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:526838 HCAPLUS
DOCUMENT NUMBER: 121:126838
TITLE: Single-stranded **DNA**-protein binding in the procyclic acidic repetitive protein (PARP) promoter of Trypanosoma brucei
AUTHOR(S): Brown, Steven Danilo; Van der Ploeg, Lex H. T.
CORPORATE SOURCE: Department of Pharmacology, Columbia University, New York, NY, 10032, USA
SOURCE: Molecular and Biochemical Parasitology (1994), 65(1), 109-22
CODEN: MBIPDP; ISSN: 0166-6851
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors performed gel retardation analyses of **DNA** -protein interactions using **DNA** from the procyclic acidic repetitive protein (PARP) promoter of the protozoan parasite Trypanosoma brucei. The PARP genes of Trypanosoma brucei are transcribed in an .alpha.-amanitin resistant manner, and it has been proposed that RNA polymerase I, rather than RNA polymerase II, transcribes the PARP genes [11]. Double-stranded **restriction fragments** contg. the essential PARP-promoter regions bound only sequence-nonspecific nuclear factors, even though protein factors that bind specifically to double-stranded **DNA** from the **snRNA** U2 promoter were present in the exts. In contrast, single-stranded **DNA** -binding proteins bound with high affinity, nucleotide-sequence and strand-specificity to the -69/-55 element and the coding and non-coding strands of the -37/-11 element.

L3 ANSWER 10 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:73973 HCAPLUS
DOCUMENT NUMBER: 120:73973
TITLE: Molecular analysis of new human endogenous retroviruses
AUTHOR(S): Sakurai, Hiroharu
CORPORATE SOURCE: Sch. Med., Hokkaido Univ., Sapporo, 060, Japan
SOURCE: Hokkaido Igaku Zasshi (1993), 68(6), 907-20
CODEN: HOIZAK; ISSN: 0367-6102
DOCUMENT TYPE: Journal
LANGUAGE: Japanese
AB The existence of many related endogenous retroviruses in human

genomes was found, by cross-hybridization with human endogenous retrovirus, ERV3 env region. The ERV3-related endogenous retroviruses also contained a variety of **restriction fragment** length polymorphism. Mol. cloning of 4 retroviral fragments among their endogenous retrovirus genomes was carried out. The 4 retroviruses were named SY-1, 2, 3, and 4, resp. A single copy of SY-1, 2, and 3 was integrated in human genome, whereas multi-copies of SY-4 were integrated. In sequence comparison, all of the 4 retroviruses were homologous with ERV3 pol-env region. SY-1 was located only on Y chromosome, and had the homologous sequence with human endogenous retrovirus NP-2 on Y chromosome. The flanking sequence of SY-1 as well as NP-2 might have an important role on investigating the origin and differentiation of Y chromosome. SY-2 was homologous with the endogenous retroviruses of not only primates but lower mammals such as mouse. It is suggested that SY-2 might be integrated into mammalian genome in early stage of the evolutional process. SY-3 was a fragments of endogenous retrovirus, contg. a sequence having homologies to U3 **small nuclear RNA** and other moderately repetitive sequences within the envelope region. SY-3 existed only in the genomes of human and rhesus monkey, but not in those of lower mammals.

L3 ANSWER 11 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:619022 HCAPLUS
DOCUMENT NUMBER: 119:219022
TITLE: Functional characterization of elements in a human U6 **small nuclear RNA** gene distal control region
AUTHOR(S): Danzeiser, Deborah A.; Urso, Olgui; Kunkel, Gary R.
CORPORATE SOURCE: Dep. Biochem. Biophys., Texas A and M Univ., College Station, TX, 77843-2128, USA
SOURCE: Molecular and Cellular Biology (1993), 13(8), 4670-8
CODEN: MCEBD4; ISSN: 0270-7306
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The promoters of vertebrate U6 **small nuclear RNA** genes contain a distal control region whose presence results in at least an eightfold level of transcriptional activation in vivo. Previous transfection expts. have demonstrated that most of the distal control region of a human U6 gene residues in a **restriction fragment** located from -244 to -149 relative to the transcriptional start site. Three octamer-related motifs that bind recombinant Oct-1 transcription factor in vitro exist in this segment of **DNA**. However, transfection of human 293 cells with various plasmid templates in which these Oct-1 binding sites had been disrupted individually or in combination showed that only the consensus octamer motif located between positions -221 to -214 was functional. Even so, the consensus octamer motif mutant template was expressed at only a moderately reduced level relative to the wild-type promoter. When another octamer-related sequence located nearby, one that did not bind Oct-1 in vitro, was disrupted along with the perfect octamer site, expression was reduced fivefold in transfected cells. A factor that binds this functional, nonconsensus octamer site (NONOCT) was detected in crude cellular exts. However, the NONOCT sequence was

not essential for activation, since its disruption caused only a 40% redn. in U6 gene expression, and mutagenesis to convert the NONOCT sequence to a consensus octamer motif restored wild-type expression. Furthermore, in vitro transcription of a human U6 proximal promoter joined to a single copy of the octamer motif was stimulated by the addn. of recombinant Oct-1 protein.

L3 ANSWER 12 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:248929 HCAPLUS
DOCUMENT NUMBER: 118:248929
TITLE: Molecular characterization in the dpy-14 region identifies the S-adenosylhomocysteine hydrolase gene in Caenorhabditis elegans
AUTHOR(S): Prasad, Shiv S.; Starr, Terence V.; Rose, Ann M.
CORPORATE SOURCE: Dep. Med. Genet., Univ. British Columbia, Vancouver, BC, V6T 1Z3, Can.
SOURCE: Genome (1993), 36(1), 57-65
CODEN: GENOE3; ISSN: 0831-2796
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The region around dpy-14 on chromosome 1 of C. elegans has been extensively studied genetically, with regard to essential gene organization. This region was one of the first for which cloned **DNA** was available as a result of **restriction fragment** length polymorphism mapping. To examine the information content of the cloned **DNA** in this region, evolutionarily conserved sequences were identified by cross-species hybridization. Ten regions of conservation have been identified and characterized with regard to mRNA abundance and **DNA** sequence. CDNAs were obtained for seven of these conserved regions and sequence from the cDNAs were used to search the SWISS protein and EMBL nucleotide data banks. Two coding regions shared **DNA** identities with existing sequences, the opa repeat family of Drosophila and the S-adenosylhomocysteine hydrolase gene. Of the three for which no corresponding cDNA were found, one corresponds to the **snRNA** U1-1. The other two did not detect transcripts on Northern anal. and are either conserved, but not coding, or code for low abundance transcripts. The d. of conserved coding regions in this study was one per 15 kbp of genomic **DNA**, three times lower than that reported on chromosome 3 by the genome sequencing project.

L3 ANSWER 13 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:241755 HCAPLUS
DOCUMENT NUMBER: 114:241755
TITLE: The U1 **snRNA** gene repeat from the sea urchin (Strongylocentrotus purpuratus): the 70 kilobase tandem repeat ends directly 3' to a U1 gene
AUTHOR(S): Yu, Jin Chen; Wendelburg, Brian; Sakallah, Sameer; Marzluff, William F.
CORPORATE SOURCE: Inst. Mol. Biophys., Florida State Univ., Tallahassee, FL, 32306, USA
SOURCE: Nucleic Acids Research (1991), 19(5), 1093-8
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Lambda phage clones contg. multiple copies of the 1.1 kb tandemly

repeated unit of the sea urchin (S. purpuratus) U1 RNA genes were isolated from a gene library. The 1.1 kb repeat unit encodes a single copy of the predominant U1 RNA expressed in oocytes and embryos prior to the blastula stage. The tandem repeat unit is about 80 kb in size and is probably present one time per haploid genome as judged by pulsed-field electrophoresis of sperm **DNA** digested with **restriction enzymes** which do not cut in the repeat unit. Two of the phage contained **DNA** flanking the repeat unit as well as several repeat units. The tandem repeat unit ends just 3' to the U1 coding region. There is only limited homol. in the 5' flanking region with U1 **snRNA** genes from the sea urchin L. variegatus.

L3 ANSWER 14 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:21729 HCAPLUS
DOCUMENT NUMBER: 114:21729
TITLE: Epstein-Barr virus **small nuclear RNAs** are not expressed in permissively infected cells in AIDS-associated leukoplakia
AUTHOR(S): Gilligan, Kevin; Rajadurai, Pathmanathan; Resnick, Lionel; Raab-Traub, Nancy
CORPORATE SOURCE: Lineberger Cancer Res. Cent., Univ. North Carolina, Chapel Hill, NC, 27599, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1990), 87(22), 8790-4
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Epstein-Barr virus (EBV) **DNA** structure and gene expression were analyzed in tissue specimens from oral hairy leukoplakia (HLP), a mucocutaneous lesion that develops in patients infected with human immunodeficiency virus (HIV). The structure of the terminal **restriction enzyme** fragments of EBV revealed that HLP is a permissive infection without a predominant, detectable population of EBV episomal **DNA**. In RNA prepns. from this uniquely permissive infection, EBV replicative mRNAs could be identified by Northern anal.; however, the virally encoded **small nuclear RNAs**, the EBERs, were not detected in most HLP RNA prepns. In situ hybridization detected EBER expression in very rare cells. These data indicate that unlike other viral **small nuclear RNAs**, the EBERs are not expressed during viral replication and must participate in the complex maintenance of latent EBV infection.

L3 ANSWER 15 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:435609 HCAPLUS
DOCUMENT NUMBER: 113:35609
TITLE: A set of U1 **snRNA**-complementary sequences involved in governing alternative RNA splicing of the kininogen genes
AUTHOR(S): Kakizuka, Akira; Ingi, Tatsuya; Murai, Toshiya; Nakanishi, Shigetada
CORPORATE SOURCE: Fac. Med., Kyoto Univ., Kyoto, 606, Japan
SOURCE: Journal of Biological Chemistry (1990), 265(17), 10102-8
CODEN: JBCHA3; ISSN: 0021-9258

DOCUMENT TYPE: Journal
LANGUAGE: English
AB The rat K and T kininogen genes show different modes of mRNA prodn. The K gene encodes 2 distinct mRNAs for high-mol.-wt. (HMW) and low-mol.-wt. (LMW) kininogens. These 2 mRNAs are generated by differential usage of the 3'-terminal exon (LMW exon) and the exon next to and upstream from the LMW exon (HMW exon) through alternative splicing and polyadenylation. In contrast, the T gene generates 1 mRNA by using selectively the LMW exon, although the T gene is extremely homologous to the K gene. A series of chimeric kininogen genes was constructed by not only exchanging equiv. **restriction fragments** of the 2 genes but also replacing nucleotides that differ between the 2 genes. The sequences and the mechanisms governing the different expression patterns of the two genes were examd. by transfecting the chimeric genes into heterologous COS cells. The results indicated that the different expression patterns of the K and T genes are governed by 2 sep. internal sequences of the HMW and LMW exons. The internal HMW sequence contains a set of 5 repetitive sequences, and these repetitive sequences are highly complementary to the 5' portion of U1 **snRNA**. Furthermore, the nucleotide differences in the U1 **snRNA**-complementary sequences between the K and T genes have marked effects on the relative formation of the HMW and LMW mRNAs; this indicates that the repetitive sequences complementary to U1 **snRNA** play a crucial role in detg. the relative expression of the 2 mRNAs. A novel mechanism is presented for alternative RNA processing, in which splicing efficiency is controlled by the interaction of U1 small nuclear ribonucleoproteins and the U1 **snRNA**-complementary repetitive sequences of the kininogen pre-mRNA.

L3 ANSWER 16 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:173481 HCAPLUS
DOCUMENT NUMBER: 112:173481
TITLE: The specific deletion and substitution mutagenesis of human U1 and U2 **snRNA** genes
AUTHOR(S): Han, Yumin
CORPORATE SOURCE: Inst. Biophys., Acad. Sin., Beijing, Peop. Rep. China
SOURCE: Shengwu Huaxue Zazhi (1990), 6(1), 66-70
CODEN: SHZAE4; ISSN: 1000-8543
DOCUMENT TYPE: Journal
LANGUAGE: Chinese
AB Oligonucleotide directed mutagenesis was used to delete a **DNA** region, flanking the human U1 and U2 **snRNA** genes, which can be bound by SV40 T antigen. Substitutions were introduced into this **DNA** region. The mutants were screened by in situ colony hybridization. The mutants were characterized by **restriction enzyme** mapping and **DNA** sequencing. The efficiency of mutagenesis was about 5%.

L3 ANSWER 17 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:49891 HCAPLUS
DOCUMENT NUMBER: 112:49891
TITLE: Octamer and SPH motifs in the U1 enhancer cooperate to activate U1 RNA gene expression
AUTHOR(S): Roebuck, Kenneth A.; Szeto, Daniel P.; Green,

Kenneth P.; Fan, Qian N.; Stumph, William E.
CORPORATE SOURCE: Mol. Biol. Inst., San Diego State Univ., San Diego, CA, 92182-0328, USA
SOURCE: Molecular and Cellular Biology (1990), 10(1), 341-52
CODEN: MCEBD4; ISSN: 0270-7306
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The transcriptional enhancer of a chicken U1 **small nuclear RNA** gene has been shown to extend over approx. 50 base pairs of **DNA** sequence located 180 to 230 base pairs upstream of the U1 transcription initiation site. It is composed of multiple functional motifs, including a GC box, an octamer motif, and a novel SPH motif. The contributions of these three distinct sequence motifs to enhancer function were studied with an oocyte expression assay. Under noncompetitive conditions in oocytes, the SPH motif is capable of stimulating U1 RNA transcription in the absence of the other functional motifs, whereas the octamer motif by itself lacks this ability. However, to form a transcription complex that is stable to challenge by a second competing **small nuclear RNA** transcription unit, both the octamer and SPH motifs are required. The GC box, although required for full enhancer activity, is not essential for stable complex formation in oocytes. Site-directed mutagenesis was used to study the **DNA** sequence requirements of the SPH motif. Functional activity of the SPH motif is spread throughout a 24-base-pair region 3' of the octamer but is particularly dependent upon sequences near an SphI **restriction site** located at the center of the SPH motif. Using embryonic chicken tissue as a source material, the authors identified and partially purified a factor, termed SBF, that binds sequence specifically to the SPH motif of the U1 enhancer. The ability of this factor to recognize and bind to mutant enhancer **DNA** fragments in vitro correlates with the functional activity of the corresponding enhancer sequences in vivo.

L3 ANSWER 18 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:181138 HCAPLUS
DOCUMENT NUMBER: 108:181138
TITLE: CDNA cloning of the human U1 **snRNA** -associated A protein: extensive homology between U1 and U2 snRNP-specific proteins
AUTHOR(S): Sillekens, Peter T. G.; Habets, Winand J.; Beijer, Ria P.; Van Venrooij, Walther J.
CORPORATE SOURCE: Dep. Biochem., Univ. Nijmegen, Nijmegen, 6500 HB, Neth.
SOURCE: EMBO Journal (1987), 6(12), 3841-8
CODEN: EMJODG; ISSN: 0261-4189
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Sera from patients with connective tissue diseases often contain antibodies against **snRNA**-assocd. proteins. Using one of these sera in an immunol. screening of a human .lambda.gt11 expression vector cDNA library, two cDNA clones for the U1 snRNP-specific A protein, termed .lambda.HA-1 and .lambda.HA-2, were isolated. Monospecific antibodies, eluted from the .beta.-galactosidase fusion protein of either clone, reacted with the U1 snRNP-specific A antigen. The identity of the clones was

confirmed by in vitro translation of hybrid selected mRNA. RNA blot anal. revealed a single polyadenylated transcript of about 1.4 kb in human cells. A cDNA of 1.2 kb, isolated from the same .lambda.gt11 expression library by cross-hybridization with a .lambda.HA-2 **restriction fragment**, covered the complete coding sequence of the A protein, as demonstrated by in vitro translation of an RNA transcript synthesized from this cDNA. The deduced amino acid sequence contains one very hydrophilic region, an internal sequence duplication, and a region highly homologous to the RNP consensus sequence that seems to be common to RNA-binding proteins. Sequence comparison with the cloned U2 snRNP-specific B" protein revealed two extremely homologous regions located in the carboxy-terminal (homol. of 86%) and amino-terminal part (homol. of 77%) of the proteins. This structural relationship indicates that proteins A and B", although located in different snRNP particles, may have identical functions.

L3 ANSWER 19 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1985:590773 HCAPLUS
DOCUMENT NUMBER: 103:190773
TITLE: Novel structure of a human U6 **snRNA** pseudogene
AUTHOR(S): Theissen, Hubert; Rinke, Jutta; Traver, Christopher N.; Luehrmann, Reinhard; Appel, Bernd
CORPORATE SOURCE: Otto-Warburg-Lab., Max-Planck-Inst. Mol. Genet., Berlin, Fed. Rep. Ger.
SOURCE: Gene (1985), 36(1-2), 195-9
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A genomic **DNA** library contg. human placental **DNA** cloned into phage .lambda. Charon 4A was screened for **snRNA** (**small nuclear RNA**) U6 genes. In vitro 32P-labeled U6 **snRNA** isolated from HeLa cells was used as a hybridization probe. A pos. clone contg. a 4.6-kb EcoRI fragment of human chromosomal **DNA** was recloned into the EcoRI site of pBR325 and mapped by restriction endonuclease digestion. **Restriction fragments** contg. U6 RNA sequences were identified by hybridization with isolated U6 [32P]RNA. The sequence anal. revealed a novel structure of a U6 RNA pseudogene, bearing 2 17-nucleotide-long direct repeats of genuine U6 RNA sequences arranged in a head-to-tail fashion within the 5' part of the mol. Hypothetical models as to how this type of **snRNA** U6 pseudogene might have been generated during evolution of the human genome are presented. When compared to mammalian U6 RNA sequences the pseudogene accounts for a 77% overall sequence homol. and contains the authentic 5'- and 3'-ends of the U6 RNA.

L3 ANSWER 20 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1984:606234 HCAPLUS
DOCUMENT NUMBER: 101:206234
TITLE: Hybridization of **snRNAs** with nuclear RNA and with rDNA **restriction fragments**
AUTHOR(S): Evtushenko, V. I.; Kurbatova, T. V.; Kozlov, A. P.

CORPORATE SOURCE: Cent. Res. Inst. Roentgenol. Radiol., Leningrad, USSR
SOURCE: Molekulyarnaya Biologiya (Moscow) (1984), 18(5), 1424-31
CODEN: MOBIBO; ISSN: 0026-8984
DOCUMENT TYPE: Journal
LANGUAGE: Russian

AB Blot hybridization of 125I- or 32P-labeled 4.5 S, U1, or U2 RNAs with EcoRI, HindIII, BamHI or SalGI **restriction fragments** of high-mol.-wt. **DNA** was performed. All 3 RNAs hybridized with fragments of ribosomal **DNA** (rDNA) and with a 5.55-kilobase BamHI fragment of rat **DNA**. U1 and 4.5 S RNAs hybridized also with 3.6-kilobase HindIII fragments. 125I-labeled U1 RNA was hybridized with nuclear RNA in formamide. Hybrid mols. which migrate in polyacrylamide gel as a broad peak slower than 28 S rRNA were formed. Thus, **small nuclear RNAs** (**snRNA**) may participate in processing and(or) splicing of heterogeneous nuclear RNA and in some other still poorly understood processes.

L3 ANSWER 21 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1984:466965 HCAPLUS
DOCUMENT NUMBER: 101:66965
TITLE: Xenopus laevis U1 **snRNA** genes: characterization of transcriptionally active genes reveals major and minor repeated gene families
AUTHOR(S): Zeller, Rolf; Carri, Maria Teresa; Mattaj, Iain W.; De Robertis, Eddy M.
CORPORATE SOURCE: Biocent., Univ. Basel, Basel, 4056, Switz.
SOURCE: EMBO Journal (1984), 3(5), 1075-81
CODEN: EMJODG; ISSN: 0261-4189
DOCUMENT TYPE: Journal
LANGUAGE: English

AB X. laevis U1 **snRNA** genes are found in several different genomic arrangements. The major family of genes is organized in tandem repeats of 1.8 kilobases (kb). The minor U1 family is much less abundant and is present on 1.2-kb HinfI **restriction fragments**. In addn., there are genomic arrangements present in 1 or very few copies, which could represent the ends of repeating units. There is no evidence for the presence of U1 pseudogenes in Xenopus. A cluster of U1 **snRNA** genes consisting of a member of the minor class of U1 **snRNA** genes and 2 of the rarely represented genes was cloned. All 3 genes were expressed upon microinjection into frog oocytes. A fragment contg. 149 base pairs (bp) of 5'-flanking sequence, the RNA coding sequence, and 27 bp of 3'-flanking sequence was accurately transcribed into U1 **snRNA**. These oocyte transcripts are assembled into specific U1 snRNPs (small nuclear ribonucleoproteins). Sequence comparison of the regions flanking Xenopus U1 and U2 **snRNA** genes showed the presence of 2 blocks of homol. that are also conserved in many other U **snRNA** genes. One of these blocks is found at position -60 to -50 before the coding sequence; its possible role in the correct initiation of transcription is discussed. The other is 3' to the coding sequence and may be involved in the accurate prodn. of mature 3' ends in the RNA.

L3 ANSWER 22 OF 29 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1984:151860 HCAPLUS
DOCUMENT NUMBER: 100:151860
TITLE: True genes for human U1 **small nuclear RNA**. Copy number, polymorphism, and methylation
AUTHOR(S): Lund, Elsebet; Dahlberg, James E.
CORPORATE SOURCE: Dep. Physiol. Chem., Univ. Wisconsin, Madison, WI, 53706, USA
SOURCE: Journal of Biological Chemistry (1984), 259(3), 2013-21
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The nucleotide sequence of a human U1 **small nuclear RNA** gene (HU1-1) is presented, along with several hundred nucleotides of its 5' and 3' flanking regions. The immediate 5' flanking region sequences are highly specific hydridization probes capable of distinguishing U1 RNA true genes from pseudogenes. The copy no. of U1 RNA genes was detd. to be const., .apprx.30/haploid genome equiv. in 6 different individuals. Nevertheless, several **restriction enzyme** cleavage site polymorphisms exist in these genes. C-C-G-G sequences in the vicinity of U1 RNA true genes are not methylated, but they are methylated near pseudogenes. Genomic **DNAs** of mouse, frog, chicken, and fruit fly contain sequences homologous to the human U1 RNA gene coding region but not to the 5' flanking region. Apparently, sequences important for expression of U1 RNA genes constitute only a minor part of the 5' flanking regions. In the HU1-1 locus, sequences similar to the consensus T-A-T-A-A-A box are located .apprx.45 and 210 base pairs upstream of the point corresponding to the 5' end of the mature RNA. Several addnl. direct repeats which may be regulatory elements are present in the upstream region. A few short, inverted repeats, which probably constitute a transcription termination signal, are in the region corresponding to the 3' end of the U1 RNA.

L3 ANSWER 23 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1983:47881 HCAPLUS
DOCUMENT NUMBER: 98:47881
TITLE: Sea urchin **small nuclear RNA** genes are organized in distinct tandemly repeating units
AUTHOR(S): Card, Charles O.; Morris, Gilbert F.; Brown, David T.; Marzluff, William F.
CORPORATE SOURCE: Dep. Chem., Florida State Univ., Tallahassee, FL, 32306, USA
SOURCE: Nucleic Acids Research (1982), 10(23), 7677-88
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The genes coding for the 2 major **small nuclear RNAs** in the sea urchin are organized in independent tandem repeating units. The **small nuclear RNAs** N1 and N2 were purified from gastrula embryos of Lytechinus variegatus. These RNAs are analogous to the U series of RNA in mammalian cells, as judged by their identical 5' termini and the sequence homol. of the N1 urchin RNA and U1 mouse RNA. These RNAs were polyadenylated with Escherichia coli adenylate transferase. A

32PO4-labeled copy of each RNA was made with RNA-dependent **DNA** polymerase. This copy was used to probe the gene organization of these RNAs by hybridization to **restriction enzyme** digests of sperm **DNA**. Each of these RNAs is encoded in a tandemly repeated cluster (.gtoreq.30 kilobases) with a repeat length of 1100-1400 bases. The N1 and N2 clusters are distinct. The N1 repeat was cloned, and the repeating organization was confirmed with the cloned gene.

L3 ANSWER 24 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1983:12339 HCAPLUS
DOCUMENT NUMBER: 98:12339
TITLE: Self-splicing RNA: autoexcision and autocyclization of the ribosomal RNA intervening sequence of Tetrahymena
AUTHOR(S): Kruger, Kelly; Grabowski, Paula J.; Zaug, Arthur J.; Sands, Julie; Gottschling, Daniel E.; Cech, Thomas R.
CORPORATE SOURCE: Dep. Chem., Univ. Colorado, Boulder, CO, 80309, USA
SOURCE: Cell (Cambridge, MA, United States) (1982), 31(1), 147-57
CODEN: CELLB5; ISSN: 0092-8674
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In the macronuclear rRNA genes of T. thermophila, a 413-base-pair intervening sequence (IVS) interrupts the 26 S rRNA coding region. A **restriction fragment** of the ribosomal **DNA** contg. the IVS and portions of the adjacent rRNA sequences (exons) was inserted downstream from the lac UV5 promoter in a recombinant plasmid. Transcription of this template by purified Escherichia coli RNA polymerase in vitro produced a shortened version of the pre-rRNA, which was then deproteinized. When incubated with monovalent and divalent cations and a guanosine factor, this RNA underwent splicing. The reactions that were characterized included the precise excision of the IVS, attachment of guanosine to the 5' end of the IVS, covalent cyclization of the IVS, and ligation of the exons. Apparently, splicing activity is intrinsic to the structure of the RNA; enzymes, **small nuclear RNAs**, and folding of the pre-rRNA into ribonucleoprotein are unnecessary for these reactions. It is proposed that the IVS portion of the RNA has several enzyme-like properties that enable it to break and reform phosphodiester bonds. The finding of autocatalytic rearrangements of RNA mols. has implications for the mechanism and the evolution of other reactions that involve RNA.

L3 ANSWER 25 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1982:576117 HCAPLUS
DOCUMENT NUMBER: 97:176117
TITLE: Assignment of **snRNA** gene sequences to the large chromosomes of rat kangaroo and Chinese hamster isolated by flow cytometric sorting
AUTHOR(S): Blin, N.; Stoehr, M.; Hutter, K. J.; Alonso, A.; Goerttler, K.
CORPORATE SOURCE: Inst. Exp. Pathol., Dtsch. Krebsforschungszent., Heidelberg, D-6900, Fed. Rep. Ger.

SOURCE: Chromosoma (1982), 85(5), 723-33
CODEN: CHROAU; ISSN: 0009-5915
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chromosomes from a rat kangaroo (Potorous tridactylus) cell line (PtK2) and from a Chinese hamster (Cricetulus griseus) cell line (CHV79) were isolated by means of fluorescence-activated flow cytometric sorting. DAPI (4'-6-Diamino-2-phenylindole) [47165-04-8] was used as the **DNA**-specific fluorescent dye. The karyotype of the PtK2 cells, which exhibits 13 chromosomes, was sepd. into 6, and the 22 chromosomes of the CHV79 cells were resolved into 11 fractions. **DNA** extd. from these chromosomal fractions was used for **restriction enzyme** digestion and blotting on nitrocellulose filters. The blots were challenged with gene probes corresponding to rRNA (18 S and 28 S) and **small nuclear RNA** (U1-**snRNA**) genes. The rRNA genes were exclusively assigned to chromosomes contg. the nucleolus organizing region (in PtK2: X chromosome; in CHV79: chromosomes 4, 5, 6, and 11). Only the largest chromosomes in both cell lines hybridized with U1-**snRNA**, indicating that these gene sequences are located on those chromosomes. Further possible genetic and biochem. applications of this exptl. system are discussed.

L3 ANSWER 26 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1982:194334 HCAPLUS
DOCUMENT NUMBER: 96:194334
TITLE: A candidate gene for human U1 RNA
AUTHOR(S): Monstein, Hans Juerg; Westin, Gunnar; Philipson, Lennart; Pettersson, Ulf
CORPORATE SOURCE: Dep. Microbiol., Univ. Uppsala, Uppsala, S-751 23, Swed.
SOURCE: EMBO Journal (1982), 1(1), 133-7
CODEN: EMJODG; ISSN: 0261-4189
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Clones contg. sequences complementary to the **small nuclear RNA** U1 were isolated from a human **DNA** library. Three clones were studied by hybridization and **restriction enzyme** cleavage. The inserts in all 3 clones were different, and each clone contained a single copy of a sequence which hybridized to U1 RNA. Only 1 of the 3 clones contained all the cleavage sites which could be predicted from the known sequence of human U1 RNA, suggesting that the 3 clones comprise 1 candidate U1 gene and 2 pseudogenes. A fragment from the recombinant with the candidate U1 gene was subcloned in plasmid pPR322, and part of its sequence was detd. The subclone contained a sequence which matched that of the human U1 RNA perfectly. The sequence TATAT, which often is found adjacent to RNA polymerase II start sites, was identified 33-37 base pairs (bp) upstream from the beginning of the U1 sequence. Two 10-bp, nearly perfect direct repeats were also identified in the vicinity of the U1 sequence. An imperfect inverted repeat followed immediately after the U1 gene.

L3 ANSWER 27 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1982:80750 HCAPLUS
DOCUMENT NUMBER: 96:80750
TITLE: Human **DNA** sequences complementary to

the **small nuclear RNA** U2

AUTHOR(S): Westin, Gunnar; Monstein, Hans Juerg; Zabielski, Jan; Philipson, Lennart; Pettersson, Ulf

CORPORATE SOURCE: Dep. Microbiol., Biomed. Cent., Uppsala, S-751 23, Swed.

SOURCE: Nucleic Acids Research (1981), 9(23), 6323-38 CODEN: NARHAD; ISSN: 0305-1048

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Clones contg. sequences complementary to the **small nuclear RNA** U2 were isolated from a human **DNA** library. Three clones, designated U2/4, U2/6, and U2/7, were purified and characterized by **restriction enzyme** cleavage, hybridization, and heteroduplex anal. Hybridization showed that the 3 clones each contained 1 single region which is complementary to U2 RNA. **Restriction enzyme** cleavage revealed that the inserted fragments in the 3 recombinants are different. Heteroduplex anal. identified a 240-380-base-pair-(bp)-long duplex region in each heteroduplex which includes sequences complementary to U2 RNA. Heteroduplexes between clones U2/4 and U2/7, as well as between U2/4 and U2/6, revealed 2 addnl. approx. 200-bp-long homologies. The remainder of the inserts lacked measurable sequence homol. Two fragments from clone U2/4 were subcloned in plasmid pBR322, and the subclones were used to det. the nucleotide sequence of a region in clone U2/4 which is complementary to U2 RNA. A comparison between the established sequence and the sequence for rat U2 RNA revealed several discrepancies.

L3 ANSWER 28 OF 29 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1981:527663 HCAPLUS

DOCUMENT NUMBER: 95:127663

TITLE: Organization of sequences related to U6 RNA in the human genome

AUTHOR(S): Hayashi, Kenshi

CORPORATE SOURCE: Biochem. Div., Natl. Cancer Cent. Res. Inst., Tokyo, Japan

SOURCE: Nucleic Acids Research (1981), 9(14), 3379-88 CODEN: NARHAD; ISSN: 0305-1048

DOCUMENT TYPE: Journal

LANGUAGE: English

AB **Small nuclear RNAs** were isolated from human placenta and fractionated into individual mol. species. They were then iodinated with 125I and used as probes to screen the human genome. Of 2 .times. 104 recombinant phage clones screened, 22 clones hybridized with U6 RNA, suggesting that there were .apprx.200 copies of this sequence family/haploid genome. Southern blots of these cloned **DNAs** digested with several **restriction enzymes** showed that each clone had only 1 fragment that carried the U6 sequence and that the lengths of these fragments varied from clone to clone, indicating that U6 sequences exist as dispersed middle repetitive **DNA**, and that the sequences surrounding these loci vary. Two of the loci and their flanking regions were subcloned into plasmid and sequenced. Both of the loci showed microheterogeneity of mainly adenine/guanine and thymine/cytosine, but had closely related sequences to U6 RNAs of rat or mouse. The divergence of the flanking regions begins

immediately outside the loci. The implications of the microheterogeneity of the U6-related sequences are discussed.

L3 ANSWER 29 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1981:1225 HCAPLUS
DOCUMENT NUMBER: 94:1225
TITLE: Dictyostelium **small nuclear RNA** D2 is homologous to rat nucleolar RNA U3 and is encoded by a dispersed multigene family
AUTHOR(S): Wise, Jo Ann; Weiner, Alan M.
CORPORATE SOURCE: Dep. Mol. Biophys. Biochem., Yale Univ., New Haven, CT, 06510, USA
SOURCE: Cell (Cambridge, MA, United States) (1980), 22(1, Pt. 1), 109-18
CODEN: CELLB5; ISSN: 0092-8674
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A 3.9 kilobase (kb) Bgl II **restriction fragment** from the genome of the cellular slime mold D. discoideum which encodes D2, the most abundant **small nuclear RNA** (**snRNA**) in vegetative amoebae, was cloned and partially sequenced. The D2 gene is colinear with the mature **snRNA** and is surrounded by extremely adenine-thymine-rich **DNA** for .gtoreq.61 nucleotides 5' to the coding region and 218 nucleotides in the 3' direction. D2 is the only small stable RNA encoded by the cloned **DNA** fragment. Although D2 RNA is homogeneous in length, a comparison of the RNA and **DNA** sequencing data indicates that cytosine/uracil or adenine/guanine heterogeneity is present in .gtoreq.3 positions within the D2 RNA sequence. Such minor heterogeneity implies that D2 is encoded by multiple genes, and indeed 5 different **restriction fragments** complementary to D2 RNA can be detected when genomic blots are probed with labeled fragments derived from the cloned D2 coding region. Further hybridization expts. using the cloned flanking sequences as probes suggest that sequences outside the RNA coding region are not detectably conserved between the 5 dispersed loci. The D2 RNA sequence is >40% homologous to the small nucleolar RNA U3B from rat Novikoff hepatoma, and the implications of this evolutionary conservation are discussed.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 11:29:57 ON 03 JUN 2003)
L4 107 S L3
L5 27 S L4 AND (CASSETTE OR LIBRAR?)
L6 19 DUP REM L5 (8 DUPLICATES REMOVED)

L6 ANSWER 1 OF 19 WPIDS (C) 2003 THOMSON DERWENT
ACCESSION NUMBER: 2002-499510 [53] WPIDS
DOC. NO. NON-CPI: N2002-395494
DOC. NO. CPI: C2002-141407
TITLE: New recombinant vector containing sequence for **small nuclear RNA**, useful e.g. for identifying variant **snRNA** that suppresses expression of transcription products.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): GRAAF, D D; LANDER, E S

PATENT ASSIGNEE(S): (WHED) WHITEHEAD INST BIOMEDICAL RES
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2002058287	A1	20020516	(200253)*		18

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2002058287	A1 Provisional	US 2000-188304P	20000310
		US 2001-804481	20010312

PRIORITY APPLN. INFO: US 2000-188304P 20000310; US 2001-804481 20010312
AN 2002-499510 [53] WPIDS
AB US2002058287 A UPAB: 20020820
NOVELTY - Recombinant vector (A) comprises **DNA** (I), consisting of an insertion **cassette** (IC) contained between at least two insertion sites (IS), that encodes a small nuclear (**sn**) **RNA** (II).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) similar recombinant vector (A1) where (I) is a **BaeI restriction fragment**;

(2) method for producing a recombinant vector comprising **DNA**, encoding a product of interest, that comprises an IC between at least two IS;

(3) cell transformed with (A);

(4) **library** of the cells of (3);

(5) method for identifying a modification of an **snRNA** that suppresses transcription;

(6) method for suppressing expression of a transcription product in a cell; and

(7) method for delivering an antisense targeting sequence into a cell nucleus.

ACTIVITY - None given in the source material.

MECHANISM OF ACTION - Inhibition of splicing or antisense inhibition of mRNA.

USE - (A) are used to identify **snRNA** modifications that inhibit expression of transcription products (and the identified **snRNA** are used to suppress expression). for delivering antisense sequences to the nucleus, and to create transgenic animals.

ADVANTAGE - (A) allow easy and directed insertion of pre-selected **DNA** modifications, i.e. faster and more efficient cloning of inserts, especially requiring only a single **restriction enzyme**, particularly one that cleaves 3' and 5' to the region being removed, eliminating problems associated with presence of extraneous nucleotides.

Dwg.0/4

L6 ANSWER 2 OF 19 WPIDS (C) 2003 THOMSON DERWENT
ACCESSION NUMBER: 2000-638139 [61] WPIDS
DOC. NO. NON-CPI: N2000-473352

DOC. NO. CPI: C2000-191876
TITLE: New nucleic acid encoding an RNA with a coding region and protein binding sites in an adjacent 5' non-coding region for translational activation of genes using the ribosome recruitment protein eIF4G.
DERWENT CLASS: B04 C06 D16 P14 S03
INVENTOR(S): DE GREGORIO, E; HENTZE, M W
PATENT ASSIGNEE(S): (EUMO-N) EURO MOLECULAR BIOLOGY LAB
COUNTRY COUNT: 85
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000053779	A1	20000914	(200061)*	EN	140
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW					
AU 9930326	A	20000928	(200067)		
EP 1159433	A1	20011205	(200203)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000053779	A1	WO 1999-EP1498	19990309
AU 9930326	A	AU 1999-30326	19990309
EP 1159433	A1	EP 1999-911756	19990309
		WO 1999-EP1498	19990309

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9930326	A	Based on	WO 200053779
EP 1159433	A1	Based on	WO 200053779

PRIORITY APPLN. INFO: US 1999-264512 19990308
AN 2000-638139 [61] WPIDS
AB WO 200053779 A UPAB: 20001128
NOVELTY - A nucleic acid (I) encoding an RNA comprising a coding region with one or more heterologous protein-binding sites (PBS) in a non-coding region 5' and adjacent to the coding region, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) RNA comprising a coding region with a PBS in a non-coding region 5' and adjacent to the coding region;
(2) a fusion protein comprising an RNA-binding protein fused to a eukaryotic translation initiation factor (eIF4E)-like protein;
(3) a fusion protein comprising an eIF4G-like protein fused to a second, different protein;
(4) a fusion protein comprising an RNA-binding protein fused to a second, different protein;
(5) nucleic acids encoding (2), (3), or (4);
(6) expression vectors comprising (I) or (5) and an origin or

replication;

(7) a population of nucleic acids, where each nucleic acid is a vector comprising an origin of replication, and a nucleotide sequence encoding (3) or (4) linked to a promoter, and where the identity of the second protein varies among the population;

(8) recombinant cells comprising (I), or (5);

(9) a transgenic organism comprising as a transgene (I) or (5);

(10) a population of recombinant cells comprising (7);

(11) producing a fusion protein comprising expressing (I), or (5) in a cell;

(12) kits comprising (I), (5) or (6) in containers, where the RNA-binding protein binds to the PBS;

(13) a nucleic acid comprising a sequence encoding an eIF4G-like protein, an RNA-binding protein or derivatives and a polylinker region 5' or 3' to the sequence that allows insertion after **restriction enzyme** digestion of a nucleic acid fragment in the correct reading frame so as to encode a fusion protein to the protein or derivative;

(14) producing a protein comprising contacting within a eukaryotic cell an RNA molecule, containing the coding region for the protein and a PBS in a noncoding region 5' and adjacent to the coding region, and an RNA-binding protein that binds to the PBS fused to an eIF4G protein;

(15) producing a protein comprising expressing an RNA binding protein that binds to the PBS fused to an eIF4G-like protein, in a eukaryotic cell containing a **DNA** molecule that is transcribed to produce an RNA containing a PBS in a region 5' and adjacent to a coding region encoding the protein;

(16) detecting an RNA-binding protein comprising recombinantly expressing an eIF4G-like protein fused to a test protein in a eukaryotic cell (C), that has **DNA** which is transcribed to produce RNA with a protein-binding site 5' and adjacent to a reporter gene coding region and detecting an increase in the protein encoded by the reporter gene, relative to the amount in the absence of the test protein;

(17) detecting a PBS in an RNA comprising expressing an eIF4G-like protein fused to a site identifying protein and an RNA containing a test sequence 5' and adjacent to a reporter gene coding region in a eukaryotic cell, and detecting an increase in the protein encoded by the reporter sequence relative to the amount in the absence of the RNA sequence;

(18) detecting binding between two proteins comprising expressing, in a (C), an eIF4G-like protein fused to the first test protein and an RNA-binding protein, that binds to the PBS, fused to the second test protein, and detecting an increase in the reporter protein relative to that in the absence of one or both test proteins;

(19) identifying a molecule that affects binding between 2 proteins comprising expressing in (C):

(i) an eIF4G-like protein fused to a protein;

(ii) an RNA-binding protein fused to a second protein; and

(iii) a candidate molecule; and detecting a change in the amount of reporter protein relative to the amount without the candidate molecule;

(20) identifying a molecule that complexes together 2 proteins comprising expressing in (C), (i), (ii) and (iii) of (19) where the 2 proteins do not bind each other and detecting an increase in the reporter protein relative to the amount without (iii);

(21) detecting protein-protein binding interactions comprising expressing in a population of (C), eIF4G-like proteins and RNA-binding proteins both fused to test proteins which vary among the population, and detecting a cell that has an increase in reporter protein compared to in the absence of the test proteins;

(22) a derivative of an eIF4G-like protein;

(23) a population of cells comprising (I) or (5);

(24) treating a disease or disorder with a protein produced in the subject by administering **DNA** that is transcribed in the subject to produce an RNA containing a PBS 5' and adjacent to the protein coding region and **DNA** that expresses an RNA-binding protein that binds the PBS, fused to an eIF4G-like protein, or a cell containing the fusion proteins; and

(25) producing a protein comprising contacting within a eukaryotic cell an RNA molecule, containing the coding region for the protein and a PBS in a noncoding region 5' and adjacent to the coding region, and an RNA-binding protein that binds to the PBS fused to a second protein that binds an eIF4g-like protein.

ACTIVITY - Antianemic; hemostatic; antiarteriosclerotic; antidiabetic; anorectic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective; antidepressant; neuroleptic; antidiabetic; cytostatic; dermatological; cardiant; virucide; antiallergic; antipsoriatic; tuberculostatic; antibacterial; immunosuppressive. No biological data is given.

MECHANISM OF ACTION - Gene therapy. No biological data is given.

USE - New methods of the invention are used for:

(1) translational activation of genes using the ribosome recruitment protein eIF4G or a similar protein;

(2) translation of RNA molecules containing PBS;

(3) identifying RNA-binding proteins, protein-protein interactions, or inhibitors or enhancers of the interactions;

(4) providing a cell or subject with therapeutic proteins;

(5) controlling the levels of translation of the therapeutic proteins;

(6) controlling the translation and stoichiometry of multiple subunit proteins;

(7) screening proteins that interact with an RNA binding site; and

(8) identifying the RNA binding sites (all claimed).

Dwg.0/9

L6 ANSWER 3 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER:	1999:17771 BIOSIS
DOCUMENT NUMBER:	PREV199900017771
TITLE:	Molecular cloning of a cDNA encoding human SPH-binding factor, a conserved protein that binds to the enhancer-like region of the U6 **small nuclear RNA** gene promoter.
AUTHOR(S):	Rincon, Julio C.; Engler, Sarah K.; Hargrove, Brian W.; Kunkel, Gary R. (1)
CORPORATE SOURCE:	(1) Dep. Biochemistry Biophysics, Texas A and M University, College Station, TX 77843-2128 USA
SOURCE:	Nucleic Acids Research, (Nov. 1, 1998) Vol. 26, No. 21, pp. 4846-4852. ISSN: 0305-1048.
DOCUMENT TYPE:	Article
LANGUAGE:	English

AB Many vertebrate **small nuclear RNA** gene promoters contain an SPH motif in their distal control regions that can confer transcriptional stimulation by RNA polymerase II or RNA polymerase III. Using the human U6 gene SPH motif as a probe, we isolated a cDNA encoding human SPH-binding factor (hSBF) from a HeLa cell expression **library**. The coding region of hSBF is almost identical to ZNF143, a 626 amino acid, seven zinc finger protein of previously unknown function. Furthermore, the predicted amino acid sequence of hSBF is highly homologous to Xenopus laevis and mouse Staf proteins, that bind to SPH motifs and stimulate transcription of selenocysteine tRNA gene promoters. Recombinant hSBF expressed in vitro or from Escherichia coli bound specifically to the human U6 gene SPH motif as shown by DNase I footprinting and electrophoretic mobility shift assays using various mutant SPH sites as competitors. Antibodies prepared against recombinant hSBF inhibited assembly of native SBF-**DNA** complexes. Immunodepleted HeLa S100 transcription extract no longer supported elevated levels of transcription by RNA polymerase III from a U6 promoter containing an SPH motif, whereas addition of recombinant hSBF protein to the immunodepleted extract reconstituted stimulated transcription.

L6 ANSWER 4 OF 19 MEDLINE
ACCESSION NUMBER: 94344764 MEDLINE
DOCUMENT NUMBER: 94344764 PubMed ID: 7520568
TITLE: The human Y4 small cytoplasmic RNA gene is controlled by upstream elements and resides on chromosome 7 with all other hY scRNA genes.
AUTHOR: Maraia R J; Sasaki-Tozawa N; Driscoll C T; Green E D; Darlington G J
CORPORATE SOURCE: Laboratory of Molecular Growth Regulation, National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, MD 20892.
CONTRACT NUMBER: DK44080 (NIDDK)
DK45285 (NIDDK)
P50-HG00201 (NHGRI)
SOURCE: NUCLEIC ACIDS RESEARCH, (1994 Aug 11) 22 (15) 3045-52.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L32608
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19941005
Last Updated on STN: 20000303
Entered Medline: 19940921

AB Ro ribonucleoproteins (RNP) constitute a class of evolutionarily conserved small cytoplasmic (sc) RNPs whose functions are unknown. In human cells four distinctive scRNAs designated hY1, hY3, hY4 and hY5 are synthesized by RNA polymerase III (pol III) and accumulate as components of Ro scRNPs. The previously isolated hY1 and hY3 genes contain upstream sequences similar to the class III promoters for U6 and 7SK **snRNAs**. Additional mammalian Y scRNA genes have been refractory to cloning due to interference from numerous hY-homologous pseudogenes and studies of hY RNA genes have been sparse. Although homologs of hY1 and hY3 RNAs exist in rodent

cells, the smaller Y4 and Y5 RNAs do not which has allowed us to localize the hY4 scRNA gene to human chromosome 7 by assaying for its transcript in rodent X human somatic cell hybrids (SCH). A chromosome 7-enriched yeast artificial chromosome (YAC) **library** was then screened and the authentic hY4 sequence was isolated by strepavidin--biotin-mediated hybrid-selection followed by poly(dA)-tailing and hemispecific PCR. The region upstream of the hY4 sequence contains a TATAAAA motif centered at -26, a candidate proximal sequence element at -63, and three octamer-like sequences located between -260 and -200. hY4 RNA is readily detectable on Northern blots after transient transfection of the hY4 gene into mouse cells but not after transfection of a construct in which the 5' flanking region was deleted. SCHs and chromosome 7-enriched YACs were used to demonstrate that all four hY RNA genes reside on human chromosome 7.

L6 ANSWER 5 OF 19 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 91212190 MEDLINE
DOCUMENT NUMBER: 91212190 PubMed ID: 2020546
TITLE: The U1 **snRNA** gene repeat from the sea urchin (Strongylocentrotus purpuratus): the 70 kilobase tandem repeat ends directly 3' to a U1 gene.
AUTHOR: Yu J C; Wendelburg B; Sakallah S; Marzluff W F
CORPORATE SOURCE: Department of Chemistry, Florida State University, Tallahassee 32306.
CONTRACT NUMBER: GM 27789 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, (1991 Mar 11) 19 (5) 1093-8. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-S62405; GENBANK-S62419; GENBANK-S62424; GENBANK-X56310; GENBANK-X56629; GENBANK-X56630; GENBANK-X56999; GENBANK-X57453; GENBANK-X57454; GENBANK-X57455
ENTRY MONTH: 199105
ENTRY DATE: Entered STN: 19910616
Last Updated on STN: 19970203
Entered Medline: 19910528

AB Lambda phage clones containing multiple copies of the 1.1 kb tandemly repeated unit of the sea urchin (S. purpuratus) U1 RNA genes were isolated from a gene **library**. The 1.1 kb repeat unit encodes a single copy of the predominant U1 RNA expressed in oocytes and embryos prior to the blastula stage. The tandem repeat unit is about 80 kb in size and is probably present one time per haploid genome as judged by pulsed-field electrophoresis of sperm **DNA** digested with **restriction enzymes** which do not cut in the repeat unit. Two of the phage contained **DNA** flanking the repeat unit as well as several repeat units. The tandem repeat unit ends just 3' to the U1 coding region. There is only limited homology in the 5' flanking region with U1 **snRNA** genes from the sea urchin L. variegatus.

L6 ANSWER 6 OF 19 MEDLINE
ACCESSION NUMBER: 87280075 MEDLINE
DOCUMENT NUMBER: 87280075 PubMed ID: 2440864

TITLE: **DNA** sequence of a human Sm autoimmune antigen. The multigene family contains a processed pseudogene.
AUTHOR: Stanford D R; Rohleder A; Neiswanger K; Wieben E D
CONTRACT NUMBER: CA 09441 (NCI)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1987 Jul 25) 262 (21) 9931-4.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J02789; GENBANK-M15918; GENBANK-M15919
ENTRY MONTH: 198709
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19970203
Entered Medline: 19870904

AB The sequence of a complementary **DNA** clone coding for a human autoimmune antigen has been determined. This **DNA** sequence predicts the amino acid sequence of a small protein ("E") which is associated with **small nuclear RNA** in human cells. Analysis of the predicted protein sequence suggests that the E protein is not closely related to other nucleic acid binding proteins. Screening of a human genomic **DNA library** has led to the isolation of several members of the E protein multigene family. Sequence analysis of one member of this family reveals that it is flanked by direct repeats and contains several mutations. One of these mutations, an insertion, terminates the long open reading frame. These features are compatible with the designation of this sequence as a processed pseudogene.

L6 ANSWER 7 OF 19 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 88111575 MEDLINE
DOCUMENT NUMBER: 88111575 PubMed ID: 2962859
TITLE: cDNA cloning of the human U1 **snRNA**-associated A protein: extensive homology between U1 and U2 snRNP-specific proteins.
AUTHOR: Sillekens P T; Habets W J; Beijer R P; van Venrooij W J
CORPORATE SOURCE: Department of Biochemistry, University of Nijmegen, The Netherlands.
SOURCE: EMBO JOURNAL, (1987 Dec 1) 6 (12) 3841-8.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X06347
ENTRY MONTH: 198803
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19970203
Entered Medline: 19880318

AB Sera from patients with connective tissue diseases often contain antibodies against **snRNA**-associated proteins. Using one of these sera in an immunological screening of a human lambda gt11 expression vector cDNA **library**, two cDNA clones for the U1 snRNP-specific A protein, termed lambda HA-1 and lambda HA-2, were

isolated. Monospecific antibodies, eluted from the beta-galactosidase fusion protein of either clone reacted with the U1 snRNP-specific A antigen. The identity of the clones was confirmed by in vitro translation of hybrid selected mRNA. RNA blot analysis revealed a single polyadenylated transcript of about 1.4 kb in human cells. A cDNA of 1.2 kb, isolated from the same lambda gt11 expression **library** by cross-hybridization with a lambda HA-2 **restriction fragment**, covered the complete coding sequence of the A protein as demonstrated by in vitro translation of an RNA transcript synthesized from this cDNA. The deduced amino acid sequence contains one very hydrophilic region, and internal sequence duplication and a region highly homologous to the RNP consensus sequence that seems to be common to RNA binding proteins. Sequence comparison with the recently cloned U2 snRNP-specific B" protein revealed two extremely homologous regions located in the carboxy-terminal (homology of 86%) and amino-terminal part (homology of 77%) of the proteins. This structural relationship indicates that proteins A and B", although located in different snRNP particles, may have identical functions.

L6 ANSWER 8 OF 19 MEDLINE
ACCESSION NUMBER: 86278133 MEDLINE
DOCUMENT NUMBER: 86278133 PubMed ID: 3015934
TITLE: Some gene variants for 5 S RNA are dispersed in the rat genome.
AUTHOR: Reddy R; Henning D; Rothblum L; Busch H
CONTRACT NUMBER: CA10893-P3 (NCI)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1986 Aug 15) 261 (23) 10618-23.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M13375; GENBANK-M13402; GENBANK-M13403
ENTRY MONTH: 198609
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19970203
Entered Medline: 19860917

AB In the course of studies on genes for **small nuclear RNAs**, seven lambda phage clones containing sequences homologous to 5 S RNA were plaque purified from a rat genomic **library**. The seven clones were found to be from six different genomic loci. When the 5 S RNA hybridized to these clones was digested by T1 RNase, only clone 5S-2 protected the RNA completely. Moreover, clone 5S-2 which has five nucleotide substitutions in the internal control region was transcribed 10 times more efficiently than a bonafide Chinese hamster 5S gene. The other clones were less efficiently transcribed than a bonafide 5S gene or not transcribed at all. The number of gene variants for 5 S RNA in the rat genome was approximately 3000. In contrast to the clustering of 5S genes and gene variants found in Xenopus, Drosophila, hamster, mouse, and human cells, the 5S gene variants in the rat genome are dispersed and most contained conserved 3'-flanking sequences. These naturally occurring 5S gene variants may be useful in binding transcription factors that affect 5S genes.

L6 ANSWER 9 OF 19 MEDLINE

ACCESSION NUMBER: 87117536 MEDLINE
DOCUMENT NUMBER: 87117536 PubMed ID: 3027665
TITLE: Functional, developmentally expressed genes for mouse U1a and U1b **snRNAs** contain both conserved and non-conserved transcription signals.
AUTHOR: Howard E F; Michael S K; Dahlberg J E; Lund E
CONTRACT NUMBER: GM 302220 (NIGMS)
S-07RR05365-25 (NCRR)
SOURCE: NUCLEIC ACIDS RESEARCH, (1986 Dec 22) 14 (24) 9811-25.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198703
ENTRY DATE: Entered STN: 19900303
Last Updated on STN: 19970203
Entered Medline: 19870306

AB Four genes that encode mouse U1a1, U1b2 and U1b6 **snRNAs** have been isolated from a mouse genomic **DNA library**. They all appear to be functional U1 genes since they are accurately transcribed into full length, capped **snRNAs** upon injection into Xenopus oocytes. A mouse pseudogene that is not transcribed in Xenopus oocytes was also isolated from the mouse genomic **library**. **DNA** sequence analysis of the 5' and 3' flanking regions of the functional genes revealed the presence of three highly conserved sequence elements that have been shown to be required for transcription initiation or 3' end formation in other U1 genes. Each of these U1 RNA genes also contains non-conserved sequences in the 5' flanking region that could function in their controlled expression during development.

L6 ANSWER 10 OF 19 MEDLINE
ACCESSION NUMBER: 86068013 MEDLINE
DOCUMENT NUMBER: 86068013 PubMed ID: 2999783
TITLE: cDNA cloning of a human autoimmune nuclear ribonucleoprotein antigen.
AUTHOR: Wieben E D; Rohleder A M; Nenninger J M; Pederson T
CONTRACT NUMBER: CA-06751 (NCI)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1985 Dec) 82 (23) 7914-8.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198601
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19970203
Entered Medline: 19860106

AB Sera from patients with systemic lupus erythematosus and other autoimmune disorders contain antibodies against nuclear proteins. One such autoantibody system, known as Sm, reacts with antigens associated with **small nuclear RNA** molecules. In this paper we report the use of Sm autoantibodies to

isolate a cDNA clone for the mRNA of one of these nuclear antigens. A HeLa cell cDNA **library** was screened by message selection followed by autoantibody reaction of cell-free translation products. This led to the identification of a cDNA clone, p281, containing sequences complementary to mRNA for an Sm autoantibody-reactive, 11,000 Mr protein. This cloned Sm antigen comigrated with the **small nuclear RNA**-associated protein known as "E" and reacted with four out of four Sm autoantibodies that precipitate E protein from total mRNA translation products. RNA gel blot hybridization with clone p281 **DNA** revealed a poly(A)+ mRNA of approximately equal to 600 nucleotides in human and marmoset (New World primate) cells. Southern blot hybridization of HeLa cell and human lymphocyte **DNA** indicated the presence of 6-10 copies of p281-homologous sequences. Similar copy numbers were observed with genomic **DNA** from baboon, cat, and mouse, indicating that the Sm antigen mRNA sequence represented in p281 is conserved across three classes of the Mammalia (primates, carnivores, and rodents). However, no cross-hybridization of p281 was observed with frog or Drosophila **DNA**. In light of existing evidence that the mammalian Sm antigen E is a weaker autoantigen than other **small nuclear RNA**-associated proteins, these results suggest a possible correlation between a protein's capacity to serve as an autoantigen during breakdown of the host's immunological tolerance and its extent of evolutionary conservation, whereas the inverse relationship applies to conventional immunity. We suspect, as have others, that this is a clue to the mechanism of autoimmunity.

L6 ANSWER 11 OF 19 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 86056956 MEDLINE
DOCUMENT NUMBER: 86056956 PubMed ID: 2998934
TITLE: Novel structure of a human U6 **snRNA** pseudogene.
AUTHOR: Theissen H; Rinke J; Traver C N; Luhrmann R; Appel B
CONTRACT NUMBER: CA 16038 (NCI)
GM 26154 (NIGMS)
SOURCE: GENE, (1985) 36 (1-2) 195-9.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-K03026
ENTRY MONTH: 198512
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19970203
Entered Medline: 19851230

AB A genomic **DNA library** containing human placental **DNA** cloned into phage lambda Charon 4A was screened for **snRNA** U6 genes. In vitro 32P-labeled U6 **snRNA** isolated from HeLa cells was used as a hybridization probe. A positive clone containing a 4.6-kb EcoRI fragment of human chromosomal **DNA** was recloned into the EcoRI site of pBR325 and mapped by restriction endonuclease digestion. **Restriction fragments** containing U6 RNA sequences were identified by hybridization with isolated U6[32P]RNA. The sequence analysis revealed a novel structure of a U6 RNA pseudogene, bearing two 17-nucleotide(nt)-long direct repeats of genuine U6 RNA

sequences arranged in a head-to-tail fashion within the 5' part of the molecule. Hypothetical models as to how this type of **snRNA** U6 pseudogene might have been generated during evolution of the human genome are presented. When compared to mammalian U6 RNA sequences the pseudogene accounts for a 77% overall sequence homology and contains the authentic 5'- and 3'-ends of the U6 RNA.

L6 ANSWER 12 OF 19 MEDLINE
ACCESSION NUMBER: 85087903 MEDLINE
DOCUMENT NUMBER: 85087903 PubMed ID: 6083546
TITLE: A complete and a truncated U1 **snRNA** gene of Drosophila melanogaster are found as inverted repeats at region 82E of the polytene chromosomes.
AUTHOR: Kejzlarova-Lepesant J; Brock H W; Moreau J; Dubertret M L; Billault A; Lepesant J A
SOURCE: NUCLEIC ACIDS RESEARCH, (1984 Dec 11) 12 (23) 8835-46.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-K03145; GENBANK-X01725
ENTRY MONTH: 198501
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19900320
Entered Medline: 19850125

AB A phage containing two sequences homologous to U1 **snRNA** was isolated from a Drosophila melanogaster genomic **library**, and identified with a previously cloned D. melanogaster U1 **snRNA** gene. **DNA** sequence analysis showed that complete and truncated U1 **snRNA** genes are present, both of which have base substitutions relative to U1 **snRNA**. These genes show conservation of 5' and 3' flanking regions relative to other U1 and U2 **snRNA** genes of Drosophila. Intramolecular renaturation experiments and electron microscope mapping demonstrates that the two U1 **snRNA** sequences are present as inverted repeats about 2.7kb apart, separated by a smaller pair of inverted repeats of an unrelated sequence. These U1 **snRNA** sequences were located by in situ hybridization at 82E, and related sequences were found at 21D and 95C on the polytene chromosome map. The results are discussed with reference to the origin and function of **snRNAs**.

L6 ANSWER 13 OF 19 MEDLINE
ACCESSION NUMBER: 84015369 MEDLINE
DOCUMENT NUMBER: 84015369 PubMed ID: 6194507
TITLE: Isolation and characterization of two linked mouse U1b **small nuclear RNA** genes.
AUTHOR: Marzluff W F; Brown D T; Lobo S; Wang S S
CONTRACT NUMBER: GM 27789 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, (1983 Sep 24) 11 (18) 6255-70.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-K03128; GENBANK-X01623; GENBANK-Y00131
ENTRY MONTH: 198311
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19970203
Entered Medline: 19831123

AB A 6.9 kilobase Eco R1 fragment containing genes for two U1 RNAs has been isolated from a **library** of mouse **DNA**. The two genes code for an RNA which is very similar, if not identical, to mouse U1b RNA as judged by S1 nuclease mapping. This RNA is one base longer than the mouse U1a RNA, human U1 RNA, and rat U1 RNA and differs in six nucleotide substitutions from rat U1 RNA. The two genes are five kilobases apart and the U1 RNAs are coded for on opposite strands of the **DNA** with the 5' ends juxtaposed. The sequences flanking the genes are identical for 700 bases 5' to the gene and at least 80 bases 3' to the gene.

L6 ANSWER 14 OF 19 MEDLINE
ACCESSION NUMBER: 83168922 MEDLINE
DOCUMENT NUMBER: 83168922 PubMed ID: 6188110
TITLE: Structural analysis of gene loci for rat U1 **small nuclear RNA**.
AUTHOR: Watanabe-Nagasu N; Itoh Y; Tani T; Okano K; Koga N; Okada N; Ohshima Y
SOURCE: NUCLEIC ACIDS RESEARCH, (1983 Mar 25) 11 (6) 1791-801.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J00800; GENBANK-K02430; GENBANK-K02431; GENBANK-K02432; GENBANK-K02433
ENTRY MONTH: 198305
ENTRY DATE: Entered STN: 19900318
Last Updated on STN: 19900318
Entered Medline: 19830505

AB Four phage clones which hybridize with U1 **small nuclear RNA** were obtained from a rat gene **library**. Two clones contain a presumed pseudogene. A third clone includes two gene candidates that are co-linear with the rat U1-RNA, 3.6kb apart and in the opposite orientation. The two genes are surrounded by identical sequences of 491bp upstream and 178bp downstream. The upstream sequences do not contain a TATA box, but share many block homologies with those for the human U1-RNA gene(1-3). A 101bp "identifier (ID) sequence", which was reported to be specifically expressed in rat brain (4), is inserted immediately after the shared sequence downstream of one of the genes. In the fourth clone, there are two putative pseudogenes, which have one or three nucleotide changes, 3kb apart and in the same orientation. Southern blot analysis of total rat **DNA** reveals about 50 U1-RNA genes/pseudogenes in the genome.

L6 ANSWER 15 OF 19 MEDLINE
ACCESSION NUMBER: 83294533 MEDLINE
DOCUMENT NUMBER: 83294533 PubMed ID: 6193279
TITLE: Molecular cloning and characterization of a gene for

rat U2 **small nuclear RNA**

AUTHOR: Tani T; Watanabe-Nagasu N; Okada N; Ohshima Y
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1983 Aug 15) 168 (3) 579-94.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-K00033; GENBANK-K00034
ENTRY MONTH: 198310
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19900319
Entered Medline: 19831008

AB Six phage clones that contain sequences hybridizable with the **small nuclear RNA** U2 were isolated from a rat gene **library**. Of these clones, one which includes a candidate for a functional U2 RNA gene was selected and characterized. The sequence within the clone which hybridizes with rat U2 RNA was completely co-linear with that of the RNA. A T-A-T-A box was not found in the region of more than 400 base-pairs which lies upstream of the gene. However, several block homologies were found with the upstream sequences of a rat U1 RNA gene candidate cloned in our laboratory. An "identifier sequence", which was reported to be an element of gene regulation related to differentiation, was found downstream of the coding region at the same distance and with the same orientation as the identifier sequence located downstream of the U1 RNA gene candidate. We detected a presumed U2 RNA precursor elongated by about 11 nucleotides at the 3' end by S1 nuclease mapping using a fragment from the clone. A potential termination signal for transcription was found within the elongated region of the presumed precursor. Southern blot analysis suggests that families of U2 RNA genes that have conserved flanking sequences are present in the genomes of rat, mouse, man, calf and chicken.

L6 ANSWER 16 OF 19 MEDLINE
ACCESSION NUMBER: 83263139 MEDLINE
DOCUMENT NUMBER: 83263139 PubMed ID: 6192042
TITLE: Isolation and characterization of three cloned fragments of human **DNA** coding for tRNAs and **small nuclear RNA** U1.
AUTHOR: Buckland R A; Cooke H J; Roy K L; Dahlberg J E; Lund E
SOURCE: GENE, (1983 May-Jun) 22 (2-3) 211-7.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198309
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19900319
Entered Medline: 19830920

AB Employing a human fetal liver **library** in lambda Charon 4A phage vector, we have isolated and characterized three clones of human **DNA** containing genes for tRNAs. One clone contains

at least three tRNA genes (tRNALys, tRNAGln and tRNALeu) within 2 kb of each other. The other two clones contain two different single genes for tRNAAsn. One of these latter two **DNAs** also contains a gene for U1 **small nuclear RNA**

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L6 ANSWER 17 OF 19 MEDLINE
ACCESSION NUMBER: 83038622 MEDLINE
DOCUMENT NUMBER: 83038622 PubMed ID: 6182525
TITLE: Mouse **DNA** sequences complementary to **small nuclear RNA** U1.
AUTHOR: Piechaczyk M; Lelay-Taha M N; Sri-Widada J; Brunel C; Liautard J P; Jeanteur P
SOURCE: NUCLEIC ACIDS RESEARCH, (1982 Aug 11) 10 (15) 4627-40.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J00645
ENTRY MONTH: 198212
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19900317
Entered Medline: 19821216

AB A mouse genomic **library** was screened for sequences complementary to U1 nuclear RNA. Out of the eight clones tested, none contained more than one copy of U1. Six of them were identical and one of those (clone 0U1-XIII) was further analyzed. This latter clone contained no other gene for discrete species of small size RNA in the 8 Kb EcoRI fragment encoding U1. A 248 bp Bg1II fragment from 0U1-XIII encompassing the full length of U1 as well as flanking regions on both sides has been subcloned and sequenced in M13 phage. Although the coding region was 96.5% homologous to rat U1a RNA, there is no direct evidence that this clone is a true gene. 3' and 5' flanking sequences of this as well as other published clones have been searched for homologies and the results of this search are discussed.

L6 ANSWER 18 OF 19 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 84182447 MEDLINE
DOCUMENT NUMBER: 84182447 PubMed ID: 6201353
TITLE: A candidate gene for human U1 RNA.
AUTHOR: Monstein H J; Westin G; Philipson L; Pettersson U
SOURCE: EMBO JOURNAL, (1982) 1 (1) 133-7.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-V00587
ENTRY MONTH: 198406
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 19900319
Entered Medline: 19840612

AB Clones containing sequences complementary to the **small nuclear RNA** U1 were isolated from the human **DNA library** of Lawn et al. (1978). Three clones

were studied by hybridization and **restriction enzyme** cleavage. The results showed that the inserts in all three clones were different and that each clone contains one single copy of a sequence which hybridizes to U1 RNA. The results revealed moreover that only one of the three clones contains all the cleavage sites which can be predicted from the known sequence of human U1 RNA, suggesting that the three clones comprise one candidate U1 gene and two pseudogenes. A fragment from the recombinant with the candidate U1 gene was subcloned in the pPR322 plasmid and part of its sequence was determined. The results showed that the subclone contains a sequence which matches that of the human U1 RNA perfectly. The sequence "TATAT" which often is found adjacent to RNA polymerase II start sites, was identified 33-37 base pairs upstream from the beginning of the U1 sequence. Two ten base pairs long, nearly perfect, direct repeats were also identified in the vicinity of the U1 sequence and an imperfect inverted repeat follows immediately after the U1 gene.

L6 ANSWER 19 OF 19 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 82105548 MEDLINE
DOCUMENT NUMBER: 82105548 PubMed ID: 6172777
TITLE: Human **DNA** sequences complementary to the **small nuclear RNA** U2.
AUTHOR: Westin G; Monstein H J; Zabielski J; Philipson L; Pettersson U
SOURCE: NUCLEIC ACIDS RESEARCH, (1981 Dec 11) 9 (23) 6323-38. Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-K03024
ENTRY MONTH: 198203
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19970203
Entered Medline: 19820313

AB Clones containing sequences complementary to the **small nuclear RNA** U2 were isolated from a human **DNA library** (1). Three clones, designated U2/4, U2/6 and U2/7 were purified and characterized by **restriction enzyme** cleavage, hybridization and heteroduplex analysis. Hybridization showed that the three clones each contained one single region which is complementary to U2 RNA. **Restriction enzyme** cleavage revealed furthermore that the inserted fragments in the three recombinants are different. Heteroduplex analysis identified a 240-380 bp long duplex region in each heteroduplex which includes sequences complementary to U2 RNA. Heteroduplexes between clones U2/4 and U2/7 as well as between U2/4 and U2/6 revealed two additional approximately 200 bp long homologies. The remainder of the inserts were found to lack measurable sequence homology. Two fragments from clone U2/4 were subcloned in the pBR322 vector and the subclones were used to determine the nucleotide sequence of a region in clone U2/4 which is complementary to U2 RNA. A comparison between the established sequence and the sequence for rat U2 RNA (2) reveals several discrepancies.

FILE 'REGISTRY' ENTERED AT 11:34:27 ON 03 JUN 2003

L7 2 S GGCCCAAGATCTCAAGGGCCCATAACATGTG/SQSN Seq ID 11

L7 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 428654-22-2 REGISTRY
CN 8: PN: US20020058287 FIGURE: 4 unclaimed sequence (9CI) (CA INDEX NAME)
SQL 59
MF Unspecified
CI MAN

REFERENCE 1: 136:396937

L7 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 428654-14-2 REGISTRY
CN 1: PN: US20020058287 FIGURE: 1A-1E unclaimed DNA (9CI) (CA INDEX NAME)
SQL 4639
MF Unspecified
CI MAN

REFERENCE 1: 136:396937

FILE 'HCAPLUS' ENTERED AT 11:36:59 ON 03 JUN 2003
L8 1 S L7
L9 0 S L8 NOT L3

FILE 'HOME' ENTERED AT 11:37:19 ON 03 JUN 2003